

1	GAT	TTT	TTG	TGA	TAT	CTT	CTT	CGG	GGG	GGG	GAA	CCT	ATT	GTA	TAA	ACG	CCA	ACC	AAC	CGG	
64	CCC	TTT	TTT	GGG	TAC	CTG	GCC	ATT	TTA	CTT	GGC	CCA	TTT	TGG	TAA	AAT	GTT	CCT	TTC	CCT	GGC
127	TTA	ATC	CCC	CTG	ATT	CCT	TGT	GGG	ATA	ACC	CGT	ATT	CCC	CCC	CTT	AGA	GTG	AAT	TTG	AAA	ACC
190	CTT	TCG	CCC	GGA	AGG	GGA	CCG	ACC	GAG	CCC	AGC	GAT	TCA	TGG	AGC	GAG	GAA	AGC	GGG	AAG	AGC
253	GCC	CAA	TAC	CCA	AGC	AGC	CTC	TCG	CCG	GCG	CGT	TGT	GCG	ATT	CAT	TAA	TAC	AGC	TGC	CAC	GAC
316	AGG	TTT	CCC	GAC	TGG	AAA	GCG	GTC	AGT	GAG	GCG	AAC	ACA	ATT	AAT	GTG	AGT	TAG	CTC	ACT	CAT
379	TAG	GCA	CCC	CAG	GCT	TTA	CAC	TTT	ATG	CTT	CCG	GCT	CGT	ATG	TTG	TGT	GGA	ATT	GTG	AGC	GGA
442	TAA	CAA	TTT	CAC	ACA	GGA	AAC	AGC	TAT	GAC	CAT	GAT	TAC	GTC	CAA	GCT	CGA	AAT	TAA	CCC	TCA
505	CTA	AAG	GGA	ACA	AAA	ACT	GGA	GCT	CCA	CCG	CGG	TGG	CGG	CCG	CTC	TAG	AAC	TAG	TGG	ATC	CCC
568	CGG	GCT	CCA	GGA	ATT	CGC	CAC	GAC	CGG	GAG	GAC	CGA	GGA	GGC	GCC	AGA	CTA	CGG	GCG	A	<u>ATG</u> MET
629	<u>GCG</u>	<u>ACC</u>	<u>CGC</u>	<u>AGC</u>	<u>CCT</u>	<u>GGC</u>	<u>GTC</u>	<u>GTG</u>	<u>ATT</u>	<u>ATG</u>	<u>GAT</u>	<u>GAT</u>	<u>TGG</u>	<u>CCA</u>	<u>GGG</u>	<u>TAT</u>	<u>GAC</u>	<u>TTG</u>	<u>AAT</u>	<u>TTA</u>	<u>TTC</u>
	Ala	Thr	Arg	Ser	Pro	Gly	Val	Val	Ile	MET	Asp	Trp	Pro	Gly	Tyr	Asp	Leu	Asn	Leu	Phe	

FIG. 1A

692 ACG TAC CCA CAG CAC TAT TAT GGA GAC TTG GAG TAT GTC CTC ATC CCT CAT GGT ATC ATT GTG
 Thr Tyr Pro Gln His Tyr Tyr Tyr Gly Asp Leu Glu Tyr Val Leu Ile Pro His Gly Ile Ile Val
 755 GAC AGA ATT GAG CGG CTG GCC AAG GAT ATT ATG AAA GAC ATA GGA TAT AGT GAC ATC ATG GTC
 Asp Arg Ile Glu Arg Leu Ala Lys Asp Ile MET Lys Asp Ile Gly Tyr Ser Asp Ile MET Val
 818 CTG TGT GTG CTT AAA GGG GGG TAC AAA TTC TGT GCT GAT CTC GTA GAA CAC CTT AAG AAC ATC
 Leu Cys Val Leu Lys Gly Gly Tyr Lys Phe Cys Ala Asp Leu Val Glu His Leu Lys Asn Ile
 881 AGC CGA AAT TCA GAT CGG TTT GTC TCA ATG AAG GTT GAT TTC ATC AGA CTA AAA AGT TAC AGG
 Ser Arg Asn Ser Asp Arg Phe Val Ser MET Lys Val Asp Phe Ile Arg Leu Lys Ser Tyr Arg
 944 AAT GAC CAG TCC ATG GGT GAG ATG CAG ATA ATC GGA GGC GGT GAT CTT TCA ACG CTG GCT GGA
 Asn Asp Gln Ser MET Gly Glu MET Gln Ile Ile Gly Gly Asp Leu Ser Thr Leu Ala Gly
 1007 AAG AAT TTT CTC ATT GTT GAG GAT GTT GTC GGA ACT GGG AGG ACC ATG AAA GCA CTA CTC AGC
 Lys Asn Phe Leu Ile Val Glu Asp Val Val Gly Thr Gly Arg Thr MET Lys Ala Leu Leu Ser
 1070 AAT ATA GAG AAA TAC AAG CCC AAC ATG ATT AAG GTA GCC AGT TTG TTG GTG AAG AGA ACA TCC
 Asn Ile Glu Lys Tyr Lys Pro Asn MET Ile Lys Val Ala Ser Leu Leu Val Lys Arg Thr Ser
 1133 AGA AGT GAC GGC TTT AGA CCT GAC TAT GCT GGA TTT GAG ATT CCA CAC TTA TTT GTG GTG GGA
 Arg Ser Asp Gly Phe Arg Pro Asp Tyr Ala Gly Phe Glu Ile Pro His Leu Phe Val Val Gly

FIG. 1B

1196 TAT GCC TTA GAT TAC AAT GAA TAC TTC AGA GAT CTG AAT CAC ATA TGC GTC ATC AAT GAG CAC
 Tyr Ala Leu Asp Tyr Asn Glu Tyr Phe Arg Asp Leu Asn His Ile Cys Val Ile Asn Glu His
 1259 GGG TAA AGG AAA ATA TCG AGT CTT AAA GAC ATG AAT TCT CAC CAC TAA AGG CCC CAG ATA GGA
 Gly STP
 1322 TCA TTT TTA CGC CTG TCT TGG GGA GCC AGT TGC AAG TTG GGC CCC CCC GGA TCT TCA TCA GGA
 1385 GG

FIG. 1C

1	MATRSPGVVISDDDEPGYDLDFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKE	56
	: . . : : : : . : : :	
1	MATRSPGVVIMDDWPGYDLNLFYTPQHYYGDLEYVLIPHGIIVDRIERLAKDIMKD	56
57	MGGHHIVALCVLKGGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSVCNDQSTG	112
	: . : . : . . : . .	
57	IGYSDIMVLCVLKGGYKFCADLVEHLKNISRNSDRFVSMKVDFIRLKSVCNDQSMG	112
113	DIKVIIGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRT	168
	::: : : : . . . : : : . . : . . . : : :	
113	EMQIIGGGDLSTLAGKNFLIVEDVVGTRGTMKALLSNIKEYKPNMIKVASLLVKRT	168
169	PRSVGYKPDFVGFEIPDKFVVGALDYNEYFRDLNHVCVISETGKAKYKA	218
	. : : : : :	
169	SRSDGFRPDYAGFEIPHLFVVGALDYNEYFRDLNHICVINEHG*RKISS	218

FIG.2

M A T R S - P G V - - - - - V I S D D E P G Y D L D L F		Majority
	10 20 30	
1	M A T R S - P G V - - - - - V I M D D W P G Y D L N L F	HPRI2b.pap
1	M A T R S - P G V - - - - - V I S D D E P G Y D L D L F	HPRI2b
1	M A T R S - P S V - - - - - V I S D D E P G Y D L D L F	HPRI2c
1	M P I P N N P G A G E N A F D P P V F V K D D D G Y D L D S F	HPRI2plas
1	M E P A C K - - - - - - - - - - Y D - - - - F	HPRI2trypan
C I P N H Y X E D L E K V L I P H G V I M D R I E R L A R D		Majority
	40 50 60	
23	T Y P Q H Y Y G D L E Y V L I P H G I I V D R I E R L A K D	HPRI2b.pap
23	C I P N H Y A E D L E R M F I P H G L I M D R T E R L A R D	HPRI2b
23	C I P N H Y V E D L E K V F I P H G V I M D R T E R L A R D	HPRI2c
31	M I P A H Y K K Y L T K V L V P N G V I K N R I E K L A Y D	HPRI2plas
10	A T S V L F T E A E L H T R M - R G V A Q R I A D D Y S N C	HPRI2trypan
V M K E M G G H I V A L C V L K G G Y K F F A D L L D H L		Majority
	70 80 90	
53	I M K D I G Y S D I M V L C V L K G G Y K F C A D L V E H L	HPRI2b.pap
53	V M K E M G G H I V A L C V L K G G Y K F F A D L L D Y I	HPRI2b
53	V M K E M G G H I V A L C V L K G G Y K F F A D L L D Y I	HPRI2c
61	I K K V Y N N E E F H I L C L K G S R G F F T A L L K H L	HPRI2plas
39	N L K P L E - N P L V I V S V L K G S F V F T A D M V R I L	HPRI2trypan

FIG.3A

	K	A	L	N	R	N	S	D	R	S	V	P	M	T	V	-	-	-	D	F	I	R	L	K	S	Y	C	N	D	Q	Majority
																100			110												
83	K	N	I	S	R	N	S	D	R	F	V	S	M	K	V	-	-	-	D	F	I	R	L	K	S	Y	R	N	D	Q	HPRT2b.pep
83	K	A	L	N	R	N	S	D	R	S	I	P	M	T	V	-	-	-	D	F	I	R	L	K	S	Y	C	N	D	Q	HPRTThu
83	K	A	L	N	R	N	S	D	R	S	I	P	M	T	V	-	-	-	D	F	I	R	L	K	S	Y	C	N	D	Q	HPRTc1
91	S	R	I	H	N	Y	S	A	V	E	M	S	K	P	L	F	G	E	H	Y	V	R	V	K	S	Y	C	N	D	Q	HPRTplas
68	G	D	F	G	-	-	-	-	-	-	V	P	T	R	V	-	-	-	E	F	L	R	A	S	S	Y	G	H	D	T	HPRTtrypan

	S	T	G	D	I	K	V	I	G	G	D	D	L	S	T	L	T	G	K	N	V	L	I	V	E	D	I	I	D	T	Majority
110	S	M	G	E	M	Q	I	I	G	G	G	D	L	S	T	L	A	G	K	N	F	L	I	V	E	D	V	V	G	T	HPRT2b.pep
110	S	T	G	D	I	K	V	I	G	G	D	D	L	S	T	L	T	G	K	N	V	L	I	V	E	D	I	I	D	T	HPRTThu
110	S	T	G	D	I	K	V	I	G	G	D	D	L	S	T	L	T	G	K	N	V	L	I	V	E	D	I	I	D	T	HPRTc1
121	S	T	G	T	L	E	I	V	S	-	E	D	L	S	C	L	K	G	K	H	V	L	I	V	E	D	I	I	D	T	HPRTplas
89	K	S	C	G	R	V	D	V	K	A	D	G	L	C	D	I	R	G	K	H	V	L	V	L	E	D	I	L	D	T	HPRTtrypan

	G	K	T	M	Q	T	L	L	S	L	V	K	K	Y	E	P	K	M	V	K	V	A	S	L	L	V	K	R	T	S	Majority
140	G	R	T	M	K	A	L	L	S	N	I	E	K	Y	K	P	N	M	I	K	V	A	S	L	L	V	K	R	T	S	HPRT2b.pep
140	G	K	T	M	Q	T	L	L	S	L	V	R	Q	Y	N	P	K	M	V	K	V	A	S	L	L	V	K	R	T	P	HPRTThu
140	G	K	T	M	Q	T	L	L	S	L	V	K	R	Y	N	P	K	M	V	K	V	A	S	L	L	V	K	R	T	S	HPRTc1
150	G	K	T	L	V	K	F	C	E	Y	L	K	K	F	E	I	K	T	V	A	I	A	C	L	F	I	K	R	T	P	HPRTplas
119	A	L	I	L	R	E	V	V	D	S	L	K	K	S	E	P	A	S	I	K	T	L	V	A	I	D	K	P	G	G	HPRTtrypan

FIG.3B

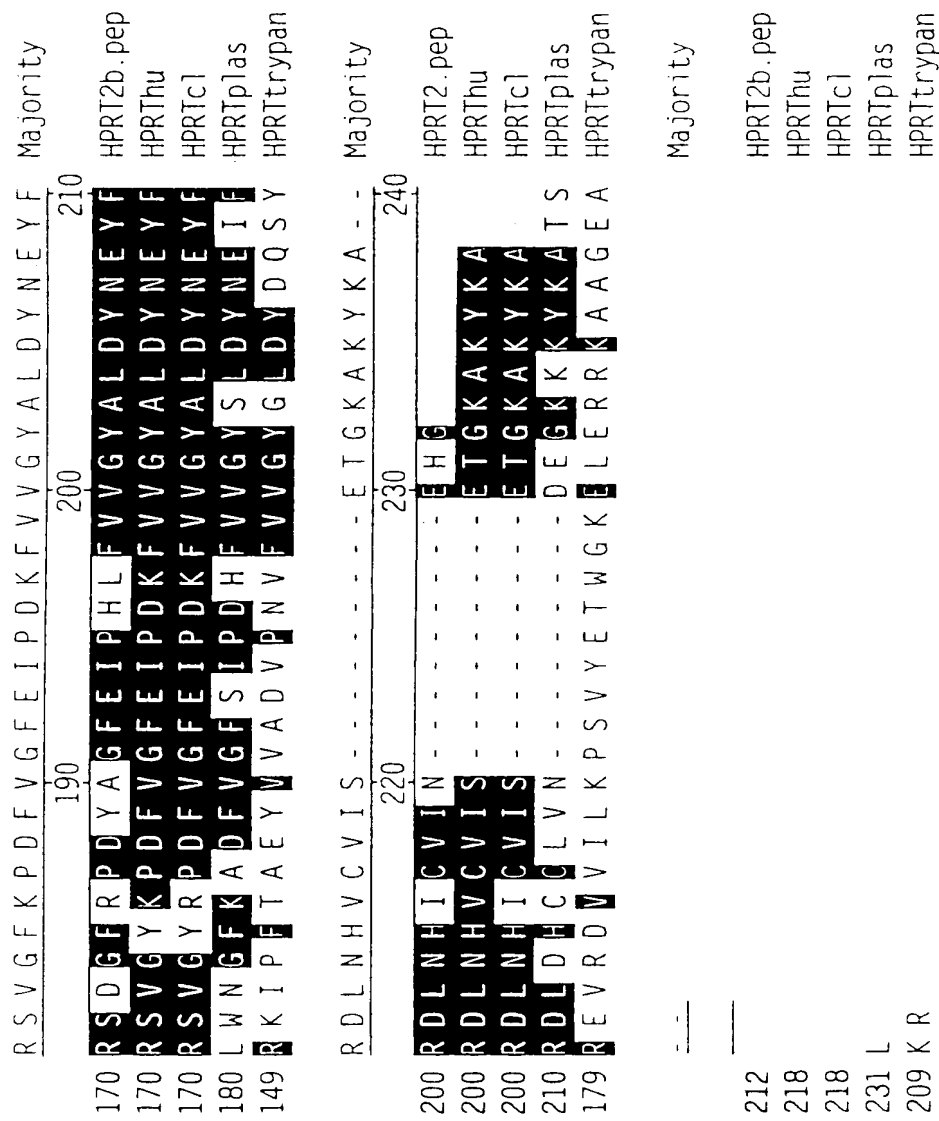


FIG.3C

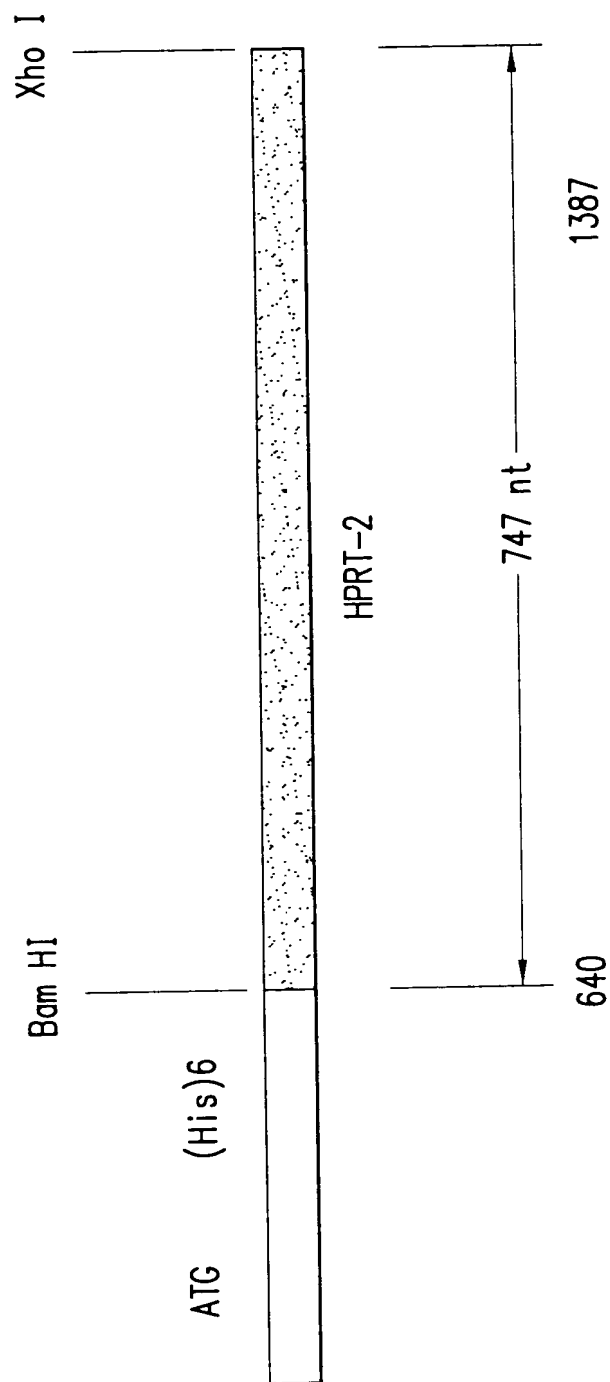


FIG.4

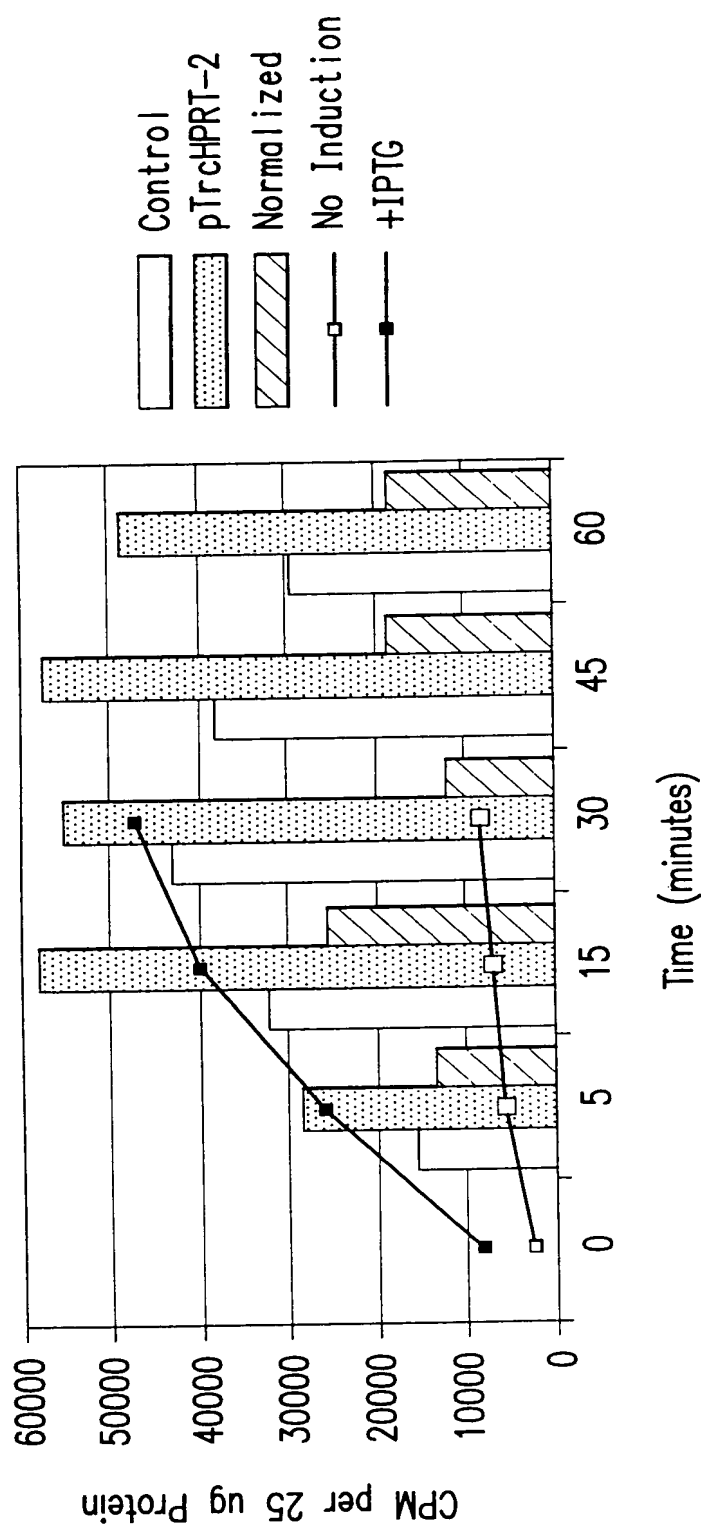


FIG.5